

GenCore version 5.1.6  
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CM nucleic - protein search, using frame\_plus\_n2p model

Run on: May 18, 2004, 17:02:11 ; Search time 0.001 Seconds  
(without alignments)  
224.316 Million cell updates/sec

Title: US-09-659-379-4  
Perfect score: 993  
Sequence: 1 CCGCGATCCGAGNATCT.....GAGAGCACTCGCGGTC 558

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2 seqs, 201 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame\_n2p model -DEV=soft -O=US09659379.seq -DB=US09659379.pcp  
-SUFFIX=ptc -OUT=compare -MINMATCH=0.1 -LOOFCU=0 -LOOPEXT=0 -UNITS=bits  
-STAR=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOALIGN=200  
-THR\_SCORE=ptc -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc  
-NORM=ext -HAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -NO\_XLPXY  
-NEG\_SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : US09659379.pcp.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	819	82.5	175	1	US-09-659-379-6
2	36	3.7	175	1	US-09-659-379-6
3	26	2.6	26	1	US-09-659-379-5
4	21	2.1	26	1	US-09-659-379-5

ALIGNMENTS

RESULT 1  
US-09-659-379-6  
Sequence 6, Application US/09659379  
GENERAL INFORMATION:  
APPLICANT: Vinik, Aaron  
Pittenger, Gary  
Rafaeloff-Phail, Ronit  
Barlow, Scott  
TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF  
INGAP IN BACTERIAL AND EUKARYOTIC CELLS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Witcoff, Ltd.

TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF  
INGAP IN BACTERIAL AND EUKARYOTIC CELLS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Witcoff, Ltd.

STREET: 1001 G Street, N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/659/379

FILING DATE: 08-Sep-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/909,725

FILING DATE: 12-AUG-1997

APPLICATION NUMBER: 08/741,096

FILING DATE: 30-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Kagan, Sarah A.

REGISTRATION NUMBER: 32,145

REFERENCE/DOCKET NUMBER: 0570.05173

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100

TELEFAX: 202-508-9299

TELEX: 97430 BME/UT

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-659-379-5

Alignment Scores:

Pred. No.: 0

Score: 21.00

Percent Similarity: 60.00%

Best Local Similarity: 60.00%

Query Match: 2.14%

DB: 1

Length: 26

Matches: 3

Conservative: 0

Mismatches: 2

Indels: 0

Gaps: 0

US-09-659-379-4 (1-558) x US-09-659-379-5 (1-26)

QY 265 TGTGAGGATCATGG 251

Db 8 CysArgMetSerTrp 12

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